Discriminating cellular heterogeneity using microwell-based RNA cytometry.

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Public Summary:

Scientific Abstract:

Discriminating cellular heterogeneity is important for understanding cellular physiology. However, it is limited by the technical difficulties of single-cell measurements. Here we develop a two-stage system to determine cellular heterogeneity. In the first stage, we perform multiplex single-cell RNA cytometry in a microwell array containing over 60,000 reaction chambers. In the second stage, we use the RNA cytometry data to determine cellular heterogeneity by providing a heterogeneity likelihood score (HLS). Moreover, we use Monte-Carlo simulation and RNA cytometry data to calculate the minimum number of cells required for detecting heterogeneity. We apply this system to characterize the RNA distributions of ageing-related genes in a highly purified mouse haematopoietic stem cell population. We identify genes that reveal novel heterogeneity of these cells. We also show that changes in expression of genes such as Birc6 during ageing can be attributed to the shift of relative portions of cells in the high-expressing subgroup versus low-expressing subgroup.

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